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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=8; day=21; hr=15; min=0; sec=34; ms=475; ]
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Application No:          10565126                  Version No:          2.0


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      Telford, John
      Bensi, Giuliano

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   STREPTOCOCCUS PYOGENES


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     Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn
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     Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys
             50                  55                  60
     Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu
     65                  70                  75                  80
     Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn
                     85                  90                  95
     His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala
                    100                 105                 110
     Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu
                    115                 120                 125
     Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu
                130                 135                 140
     Leu His Asn Ala Gln Ala Asp Gln His Ser Lys Glu Thr Ala Leu Ser
     145                 150                 155                 160
     Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu
                    165                 170                 175
     Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala
                    180                 185                 190

Met Ile Ser Asn Pro Asp Ala Ile Thr Lys Ala Ala Gln Thr Ala Asn
        195                 200                 205
Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu Glu Lys Ala Lys Ala Asp
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Leu Glu Asn Gln Lys Ala Lys Val Lys Lys Gln Leu Thr Glu Glu Leu
225                 230                 235                 240
Ala Ala Gln Lys Ala Ala Leu Ala Glu Lys Glu Ala Glu Leu Ser Arg
                245                 250                 255
Leu Lys Ser Ser Ala Pro Ser Thr Gln Asp Ser Ile Val Gly Asn Asn
                260                 265                 270
Thr Met Lys Ala Pro Gln Gly Tyr Pro Leu Glu Glu Leu Lys Lys Leu
        275                 280                 285
Glu Ala Ser Gly Tyr Ile Gly Ser Ala Ser Tyr Asn Asn Tyr Tyr Lys
        290                 295                 300
Glu His Ala Asp Gln Ile Ile Ala Lys Ala Ser Pro Gly Asn Gln Leu
305                 310                 315                 320
Asn Gln Tyr Gln Asp Ile Pro Ala Asp Arg Asn Arg Phe Val Asp Pro
                325                 330                 335
Asp Asn Leu Thr Pro Glu Val Gln Asn Glu Leu Ala Gln Phe Ala Ala
                340                 345                 350
His Met Ile Asn Ser Val Arg Arg Gln Leu Gly Leu Pro Pro Val Thr
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Val Thr Ala Gly Ser Gln Glu Phe Ala Arg Leu Leu Ser Thr Ser Tyr
        370                 375                 380
Lys Lys Thr His Gly Asn Thr Arg Pro Ser Phe Val Tyr Gly Gln Pro
385                 390                 395                 400
Gly Val Ser Gly His Tyr Gly Val Gly Pro His Asp Lys Thr Ile Ile
                405                 410                 415
Glu Asp Ser Ala Gly Ala Ser Gly Leu Ile Arg Asn Asp Asp Asn Met
                420                 425                 430
Tyr Glu Asn Ile Gly Ala Phe Asn Asp Val His Thr Val Asn Gly Ile
        435                 440                 445
Lys Arg Gly Ile Tyr Asp Ser Ile Lys Tyr Met Leu Phe Thr Asp His
        450                 455                 460
Leu His Gly Asn Thr Tyr Gly His Ala Ile Asn Phe Leu Arg Val Asp
465                 470                 475                 480
Lys His Asn Pro Asn Ala Pro Val Tyr Leu Gly Phe Ser Thr Ser Asn
                485                 490                 495
Val Gly Ser Leu Asn Glu His Phe Val Met Phe Pro Glu Ser Asn Ile
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Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala Ala Leu His Gln Thr Glu
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Ala Leu Ala Glu Gln Ala Ala Ala Arg Val Thr Ala Leu Val Ala Lys

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      Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg
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      Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala
                   675              680              685
      Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu
              690              695              700
      Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His
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      Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His
                   725              730              735
      Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro
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      Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro
                   755              760              765
      Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser
              770              775              780
      Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val
      785              790              795              800
      Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile
                   805              810              815
      Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly
                   820              825              830
      Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln
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tcaggagaaa cgaaggcgag taatactcac gacgatagtt taccaaaacc agaaacaatt       180
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cagcaagata tgaacaaaa agctttaacc tctgcacaag aaatttacac taatactctt       360
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gaacaaaaag ctagcatttc agcagaaact actcgagctc aagatttagt ggaacaagtc       540
aaaacgtctg aacaaaatat tgctaagctc aatgctatga ttagcaatcc tgatgctatc       600
actaaagcag ctcaaacggc taatgataat acaaaagcat taagctcaga attggagaag       660
gctaaagctg acttagaaaa tcaaaaagct aaagttaaaa agcaattgac tgaagagttg       720
gcagctcaga aagctgctct agcagaaaaa gaggcagaac ttagtcgtct taaatcctca       780
gctccgtcta ctcaagatag cattgtgggt aataatacca tgaaagcacc gcaaggctat       840
cctcttgaag aacttaaaaa attagaagct agtggttata ttggatcagc tagttacaat       900
aattattaca aagagcatgc agatcaaatt attgccaaag ctagtccagg taatcaatta       960
aatcaatacc aagatattcc agcagatcgt aatcgctttg ttgatcccga taatttgaca      1020
ccagaagtgc aaaatgagct agcgcagttt gcagctcaca tgattaatag tgtaagaaga      1080
caattaggtc taccaccagt tactgttaca gcaggatcac aagaatttgc aagattactt      1140
agtaccagct ataagaaaac tcatggtaat acaagaccat catttgtcta cggacagcca      1200
ggggtatcag ggcattatgg tgttgggcct catgataaaa ctattattga agactctgcc      1260
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tttacagatc atttacacgg aaatacatac ggccatgcta ttaacttttt acgtgtagat         1440
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caatatctaa gggactttaa attgaatcct aaccgccttc aagtgatacg tgagcgcatt         2040
gataatacta agcaagattt ggctaaaact acctcatctt tgttaaatgc acaagaagct         2100
ttagcagcct tacaagctaa acaaagcagt ctagaagcta ctattgctac cacagaacac         2160
cagttgactt tgcttaaaac cttagctaac gaaaaggaat atcgccactt agacgaagat         2220
atagctactg tgcctgattt gcaagtagct ccacctctta cgggcgtaaa accgctatca         2280
tatagtaaga tagatactac tccgcttgtt caagaaatgg ttaaagaaac gaaacaacta         2340
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actcagccct catctaagac atcttatggc tcaggatctt ctacaacgag caatctcatt         2520
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    Thr Ile Gln Glu Ala Lys Ala Thr Ile Asp Ala Val Glu Lys Thr Leu
            35                  40                  45
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Ser Gln Gln Lys Ala Glu Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys
        50                    55                    60
Thr Thr Ala Glu Ile Asn His Leu Lys Glu Gln Gln Asp Asn Glu Gln
65                    70                    75                    80
Lys Ala Leu Thr Ser Ala Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser
                85                    90                    95
Ser Glu Glu Thr Leu Leu Ala Gln Gly Ala Glu His Gln Arg Glu Leu
                100                   105                   110
Thr Ala Thr Glu Thr Glu Leu His Asn Ala Gln Ala Asp Gln His Ser
                115                   120                   125
Lys Glu Thr Ala Leu Ser Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr
        130                   135                   140
Thr Arg Ala Gln Asp Leu Val Glu Gln Val Lys Thr Ser Glu Gln Asn
145                   150                   155                   160
Ile Ala Lys Leu Asn Ala Met Ile Ser Asn Pro Asp Ala Ile Thr Lys
                165                   170                   175
Ala Ala Gln Thr Ala Asn Asp Asn Thr Lys Ala Leu Ser Ser Glu Leu
                180                   185                   190
Glu Lys Ala Lys Ala Asp Leu Glu Asn Gln Lys Ala Lys Val Lys Lys
                195                   200                   205
Gln Leu Thr Glu Glu Leu Ala Ala Gln Lys Ala Ala Leu Ala Glu Lys
        210                   215                   220
Glu Ala Glu Leu Ser Arg Leu Lys Ser Ser Ala Pro Ser Thr Gln Asp
225                   230                   235                   240
Ser Ile Val Gly Asn Asn Thr Met Lys Ala Pro Gln Gly Tyr Pro Leu
                245                   250                   255
Glu Glu Leu Lys Lys Leu Glu Ala Ser Gly Tyr Ile Gly Ser Ala Ser
                260                   265                   270
Tyr Asn Asn Tyr Tyr Lys Glu His Ala Asp Gln Ile Ile Ala Lys Ala
                275                   280                   285
Ser Pro Gly Asn Gln Leu Asn Gln Tyr Gln Asp Ile Pro Ala Asp Arg
        290                   295                   300
Asn Arg Phe Val Asp Pro Asp Asn Leu Thr Pro Glu Val Gln Asn Glu
305                   310                   315                   320
Leu Ala Gln Phe Ala Ala His Met Ile Asn Ser Val Arg Arg Gln Leu
                325                   330                   335
Gly Leu Pro Pro Val Thr Val Thr Ala Gly Ser Gln Glu Phe Ala Arg
                340                   345                   350
Leu Leu Ser Thr Ser Tyr Lys Lys Thr His Gly Asn Thr Arg Pro Ser
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Phe Val Tyr Gly Gln Pro Gly Val Ser Gly His Tyr Gly Val Gly Pro
        370                   375                   380
His Asp Lys Thr Ile Ile Glu Asp Ser Ala Gly Ala Ser Gly Leu Ile
385                   390                   395                   400
Arg Asn Asp Asp Asn Met Tyr Glu Asn Ile Gly Ala Phe Asn Asp Val
                405                   410                   415
His Thr Val Asn Gly Ile Lys Arg Gly Ile Tyr Asp Ser Ile Lys Tyr
                420                   425                   430
Met Leu Phe Thr Asp His Leu His Gly Asn Thr Tyr Gly His Ala Ile
                435                   440                   445
Asn Phe Leu Arg Val Asp Lys His Asn Pro Asn Ala Pro Val Tyr Leu
        450                   455                   460
Gly Phe Ser Thr Ser Asn Val Gly Ser Leu Asn Glu His Phe Val Met
465                   470                   475                   480
Phe Pro Glu Ser Asn Ile Ala Asn His Gln Arg Phe Asn Lys Thr Pro
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Ile Lys Ala Val Gly Ser Thr Lys Asp Tyr Ala Gln Arg Val Gly Thr

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Ala Lys Val Ser Gln Leu Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln
545                      550                      555                      560
Ser Asp Ser Leu Asn Leu Gln Val Arg Gln Leu Asn Asp Thr Lys Gly
                565                      570                      575
Ser Leu Arg Thr Glu Leu Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu
        580                      585                      590
Glu Ala Thr Arg Asp Gln Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala
        595                      600                      605
Ala Leu His Gln Thr Glu Ala Leu Ala Glu Gln Ala Ala Ala Arg Val
        610                      615                      620
Thr Ala Leu Val Ala Lys Lys Ala His Leu Gln Tyr Leu Arg Asp Phe
625                      630                      635                      640
Lys Leu Asn Pro Asn Arg Leu Gln Val Ile Arg Glu Arg Ile Asp Asn
                645                      650                      655
Thr Lys Gln Asp Leu Ala Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln
                660                      665                      670
Glu Ala Leu Ala Ala Leu Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr
                675                      680                      685
Ile Ala Thr Thr Glu His Gln Leu Thr Leu Leu Lys Thr Leu Ala Asn
        690                      695                      700
Glu Lys Glu Tyr Arg His Leu Asp Glu Asp Ile Ala Thr Val Pro Asp
705                      710                      715                      720
Leu Gln Val Ala Pro Pro Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser
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